High Level gene expression Analysis. Functional Annotation and Pathway Analysis

Today's Outline

Part A :   Allocation of projects
                   Class activity

Break – 10 min

Part B :   Guest Lecture – Prof Neil Lawrence

                   Discussion

Class activity: Discussion based on your questions from lecture material

Today's Learning

- What are the project that will be allocated to you for the final assignment

- Critical discussion of the module material

- What machine learning can do for us

- The importance of modelling in biology

What are the learning outcomes of this module?

This module aims to:

1. provide an understanding of the *fundamental concepts* and technologies underlying computational biology and bioinformatics

2. it is aimed at biology students with basic knowledge of *mathematical concepts*, to equip them with methods of Bioinformatics and Computational biology for the analysis of biological data

3. provide skills in experimental design and data pipeline generation

4. it will use a *multidisciplinary* approach integrated with programming tools and statistical concepts underpinning advanced data analysis and methods that are suitable *for high-throughput data analysis*

5. provide new transferable skills

BMS353 assessment

The exam for this module will be split in two parts:

Part A – A Multiple Choice Question test for the duration of 1hr, that will count 30% of the final grade

Part B – A notebook with the implementation of allocated projects that will count for 70% of the final grade.

The project will be a collection of all the tools experienced in the practical labs implemented on a set of real data. It will be developed in groups of three students, but notebook will have to be handed individually.

MCQ assessment:

Each question will have 4 possible responses A, B, C or D. **<u>ONLY ONE RESPONSE IS CORRECT IN EACH CASE.</u>** Each question is worth one mark, correct answer will count as 1, an incorrect answer will count as -0.5. **Not answered questions will count as 0**.

The Projects

- They are analysis of gene expression microarray data of research project that have been published.

- The data is all produced here in Sheffield

- The samples are human cell lines or primary culture of human cells.

- All are related to clinical applications.

Project A

This study is to explain the effect od the transcription factor SP1 in colon cells. To elucidate this effect a colon cell line was used and a silencing of the transcription factor SP1 was obtained using RNAi techniques *in vitro*. A gene expression profile of the cells with SP1 silencing and without silencing was done after 48hrs in culture.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:
* M48-1.CEL   control at 48hrs in culture - sample 1
* M48-2.CEL   control at 48hrs in culture - sample 2
* S48-1.CEL   SP1 silenced at 48hrs in culture - sample 1
* S48-2.CEL   SP1 silenced at 48hrs in culture - sample 2

After estimating gene expression, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the silencing of SP1 might have altered.

Project B

This study is to explain the effect od the transcription facto SP1 in colon cells. To elucidate this effect a colon cell line was used and a silencing of the transcription factor SP1 was obtained using RNAi techniques in *vitro*. A gene expression profile of the cells with SP1 silencing and without silencing was done after 72hrs in culture.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:
* M72-1.CEL   control at 72hrs in culture - sample 1
* M72-2.CEL   control at 72hrs in culture - sample 2
* S72-1.CEL   SP1 silenced at 72hrs in culture - sample 1
* S72-2.CEL   SP1 silenced at 72hrs in culture - sample 2

After estimating gene expression, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the silencing of SP1 might have altered.

Project C

This study is to explain the effect of Hypoxia on human Neutrophils to identify possible involvement of inflammatory response in adverse prognosis of hypoxia-related disease, i.e. pulmonary hypertension, myocardial infarction. To elucidate this effect primary cultures of human neutrophils were studied at normal condition and in a hypoxia condition. A gene expression profile of the neutrophil in normal and hypoxia condition was done after certain amount of hrs in culture.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2.
The files containing the data are as follow:
* LPGMa.CEL   neutrophils at normal condition in culture - sample 1
* LPGMb.CEL   neutrophils at normal condition in culture - sample 2
* LPHa.CEL   neutrophils with hypoxia induced in culture - sample 1
* LPHb.CEL   neutrophils with hypoxia induced in culture - sample 2

After estimating gene expression levels, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the hypoxia might have altered in neutrophils.